

OIPE

DATE: 11/20/2001 RAW SEQUENCE LISTING TIME: 19:11:34 PATENT APPLICATION: US/09/836,470

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\1836470.raw

SEQUENCE LISTING

ENTERED

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Witte, Owen N.
     5
                            Weng, Zhigang
           (ii) TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED
     6
                                     RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN
     8
                                     TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS
     9
    10
           (iii) NUMBER OF SEQUENCES: 40
    12
            (iv) CORRESPONDENCE ADDRESS:
    14
                  (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
    15
                  (B) STREET: 620 Newport Center Drive, 16th Floor
    16
                  (C) CITY: Newport Beach
    17
                  (D) STATE: CA
    18
                  (E) COUNTRY: U.S.A.
     19
                  (F) ZIP: 92660
     20
             (V) COMPUTER READABLE FORM:
     22
                  (A) MEDIUM TYPE: Diskette
     23
                  (B) COMPUTER: IBM Compatible
     24
                   (C) OPERATING SYSTEM: DOS
     25
                  (D) SOFTWARE: FastSEQ for Windows Version 2.0
     26
            (vi) CURRENT APPLICATION DATA:
     28
                   (A) APPLICATION NUMBER: US/09/836,470
C--> 29
                   (B) FILING DATE: 18-Apr-2001
C--> 30
                   (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
     33
                   (A) APPLICATION NUMBER: US/08/969,815
     34
                   (B) FILING DATE:
     35
          (viii) ATTORNEY/AGENT INFORMATION:
     37
                   (A) NAME: Bartfeld, Neil S
     38
                   (B) REGISTRATION NUMBER: 39,901
     39
                   (C) REFERENCE/DOCKET NUMBER: UCLA015.001A
     40
             (ix) TELECOMMUNICATION INFORMATION:
     42
                   (A) TELEPHONE: 619-235-8550
     43
                   (B) TELEFAX: 619-235-0176
     44
                   (C) TELEX:
     45
     48 (2) INFORMATION FOR SEQ ID NO: 1:
              (i) SEQUENCE CHARACTERISTICS:
     50
                   (A) LENGTH: 1507 base pairs
     51
                   (B) TYPE: nucleic acid
     52
                   (C) STRANDEDNESS: single
      53
                   (D) TOPOLOGY: linear
      54
             (ii) MOLECULE TYPE: CDNA
      56
             (ix) FEATURE:
      57
                   (A) NAME/KEY: Coding Sequence
      59
                    (B) LOCATION: 147...1292
      60
                    (D) OTHER INFORMATION:
      61
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
      63
```





RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,470

DATE: 11/20/2001 TIME: 19:11:34

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\1836470.raw

	Output Book In (
	AAACCTCCCA GCTGGGCCTG CAGAGGGGTG CT	CAGCCCTG CCTCAGGACG GGCCTGCCCT	60
65		AGCTGCCA GAGCCACCTT CACAMOOGG	120
66	TOTAL CARROL WORLD CAMPAGGA GCCACC ATG AS	A TCA GAA CCI ACC AAI GOII GOII	173
67	Mot A	rg Ser Glu Pro Thr Asn Ala Ala	
68	1	5	
69	and add ada cmc ccc cmm acc mc	C GTT CTT CAG AGC ACC TCA GTA	221
71		r val Leu Gill Sei illi Sei var	
72 73	15	20	0.60
75	TO THE TANK THE CASE ASSET THE CASE STEET TO	C TAC GAG GAG AGC AGA GTG GTC	269
75 76	- al. mbm Cvc Uic Val Se	r Tyr Giu Giu Sei Rig vai vai	
70 77	2.0	33	217
77 79	THE STEE STEE STEE THE ACT SET SET STEE TG	C CTG CTG GGC CTA CCA GCC AAC	317
80	1 - 1 m Com Xla Val CV	s Leu Leu Gly Leu Flo Alu Aba	
81	45 50	55	265
83	and row coo mee ere ree CTG CTG	G CAA GTC CTG CAG AGG AAC GTG	365
84	- mb - 31 mm Lou Thr Lell Le	u Gin vai Leu Gin Aig Abh vai	
85	- ረላ ክን	70	112
87	, ama mad dmc mmc mcc cmc TC	C CTC TGT GAG CTG CTC TAC ATC	413
88	I man I ou Dho Cuc I ell Se	r Leu Cys Giu Leu Leu 171 110	
89	. ar 80	6.5	461
91	THE TAR AND GON MIND THE ATE ATE TO	C ATC CAG AAT CAG CAC AAA TGG	401
92	I now Tou Tro Tle Tle TV	r lie din Ash din his hys iip	
93	05	100	509
95	3 90 5 AAC CTG GGT CCG CAG GCC TGC AAG GT	G ACT GCT TAC ATC TTC TIC TGC	303
96	11- 11- Circ WC Va	II THE ALC THE THE THE THE	
97	_ 110	115	557
99	7 9 AAC ATC TAC ATC AGC ATC CTC TTG CT	C TGC TGC ATT TCC TGC GAC COC	
100		led Cys Cys Tie Sei Cys Hop 1125	
10	01 125		605
10	01 123 03 TAC ATG GCC GTG GTC TAT GCA CTG	The Sor Arg Glv His Arg His Gln	
10		150	
10	05 140 145 07 AGG ACT GCT GTC ACC ATT TCT GCG		653
10	07 AGG ACT GCT GTC ACC ATT ICI GCG 108 Arg Thr Ala Val Thr Ile Ser Ala	Tys Val The Leu Leu Val Gly Leu	
10	08 Arg Thr Ala Val Thr lie Ser Ala	JyB .Vul 110 200	
	160	165	
10	160	103	701
11	09 155 160	AAG GTG GAG AAG AGT TTC TGC TTT	701
11 11	09 155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180	701
11 11 11	155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 185 ATA GCC GGC TAC CAC TAC CTG CGT	701 749
11 11 11 11	155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 185 ATA GCC GGC TAC CAC TAC CTG CGT	
11 11 11 11	155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 185 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 200	749
11 11 11 11 11	155 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 180 190	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 185 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 200 CTC GGC ATC CTG GCG TTC ACC AAT	
11 11 11 11 11 11	155 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 180 190	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 185 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 200 CTC GGC ATC CTG GCG TTC ACC AAT	749
11 11 11 11 11 11 11	09 155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 19 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 CTC GGC ATC CTG GCG TTC ACC AAT Leu Gly Ile Leu Ala Phe Thr Asn 210	749 797
11 11 11 11 11 11 11 12	155 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 19 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro 205	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 CTC GGC ATC CTG GCG TTC ACC AAT Leu Gly Ile Leu Ala Phe Thr Asn 210 CTC AGT GAC AGC CTG AGC GCT GCG	749
11 11 11 11 11 11 11 12 12	155 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 19 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro 205	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 CTC GGC ATC CTG GCG TTC ACC AAT Leu Gly Ile Leu Ala Phe Thr Asn 210 CTC AGT GAC AGC CTG AGC GCT GCG	749 797
11 11 11 11 11 11 11 12 12	09 155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 190 17 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro 205 225 CAC CAG ATC TTC CGG AGC ATC AAA 24 His Gln Ile Phe Arg Ser Ile Lys	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe	749 797 845
11 11 11 11 11 11 12 12 12 12	155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 190 177 19 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro 21 205 225 CAC CAG ATC TTC CGG AGC ATC AAA 124 His Gln Ile Phe Arg Ser Ile Lys 225	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 CTC GGC ATC CTG GCG TTC ACC AAT Leu Gly Ile Leu Ala Phe Thr Asn 210 CTC AGT GAC AGC CTG AGC GCT GCG Leu Ser Asp Ser Leu Ser Ala Ala 230 GCC ATC GCG GTC GTC ACC ATC TTC	749 797
11 11 11 11 11 11 12 12 12 12	09 155 160 11 GTT AAC TAT CCA GTG TTT GAC ATG 12 Val Asn Tyr Pro Val Phe Asp Met 13 170 175 15 GAG CCC CTG AGG ATG AAC AGC AAG 16 Glu Pro Leu Arg Met Asn Ser Lys 17 19 TTC ACC TTT GGC TTT GCC ATC CCT 20 Phe Thr Phe Gly Phe Ala Ile Pro 21 205 22 CAC CAG ATC TTC CGG AGC ATC AAA 124 His Gln Ile Phe Arg Ser Ile Lys	AAG GTG GAG AAG AGT TTC TGC TTT Lys Val Glu Lys Ser Phe Cys Phe 180 ATA GCC GGC TAC CAC TAC CTG CGT Ile Ala Gly Tyr His Tyr Leu Arg 195 CTC GGC ATC CTG GCG TTC ACC AAT Leu Gly Ile Leu Ala Phe Thr Asn 210 CTC AGT GAC AGC CTG AGC GCT GCG Leu Ser Asp Ser Leu Ser Ala Ala 230 GCC ATC GCG GTC GTC ACC ATC TTC	749 797 845





DATE: 11/20/2001 RAW SEQUENCE LISTING TIME: 19:11:34 PATENT APPLICATION: US/09/836,470

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\I836470.raw

129		235					240					245					
131	CTG		TGC	TTT	GCT	CCC	TAC	CAC	GTG	GTA	CTC	CTC	GTC	AAA	GCT	GCC	941
132	Leu	Val	Cys	Phe	Ala	Pro	Tyr	His	Val	Val	Leu	Leu	Val	Lys	Ala	Ala	
133	250		- 4			255	-				260					265	
135	AGC	TTT	TCC	TTC	TAC	CAA	GGA	GAC	ATG	GAT	GCC	GTG	TGT	GCC	TTT	GAA	989
136	Ser	Phe	Ser	Phe	Tyr	Gln	Gly	Asp	Met	Asp	Ala	Val	Cys	Ala	Phe	Glu	
137					270					275					280		
139	AGC	AGA	CTG	TAC	ACA	GTC	TCT	ATG	GTG	TTT	CTG	TGC	CTG	TCT	ACA	GTC	1037
140	Ser	Arg	Leu	Tyr	Thr	Val	Ser	Met	Val	Phe	Leu	Cys	Leu	Ser	Thr	Val	
141		_		285					290					295			
143	AAC	AGT	GTG	GCT	GAC	CCC	ATC	ATC	TAC	GTG	CTG	GGT	ACA	GAC	CAC	TCT	1085
144	Asn	Ser	Val	Ala	Asp	Pro	Ile	Ile	Tyr	Val	Leu	Gly		Asp	His	Ser	
145		•	300					305					310				4400
147	CGG	CAA	GAA	GTG	TCC	AGA	ATC	CAC	ACA	GGG	TGG	AAA	AAG	TGG	TCC	ACA	1133
148	Arg	Gln	Glu	Val	Ser	Arg	Ile	His	Thr	Gly	${\tt Trp}$		Lys	\mathtt{Trp}	Ser	Thr	
149		315					320					325					1101
151	AAG	ACA	TAT	GTT	ACA	TGC	TCA	AAG	GAC	TCT	GAG	GAG	ACA	CAC	TTG	ccc	1181
152	Lys	Thr	Tyr	Val	Thr	Cys	Ser	Lys	Asp	Ser		Glu	Thr	His	Leu	Pro	
153	330					335					340	~~~	000	63.6	COT	345	1220
155	ACA	GAG	CTT	TCA	AAC	ACA	TAC	ACC	TTC	CCC	AAT	CCC	GCG	CAC	CCT	Dma	1229
156	Thr	Glu	Leu	Ser		Thr	Tyr	Thr	Phe		Asn	Pro	Ата	HIS	Pro	Pro	
157					350					355	maa	maa	003	CAC	360	CTC	1277
159	GGA	TCA	CAG	CCA	GCG	AAG	CTA	GGT	TTA	CTG	TGC	TCG	DTO	GAG	AGA Ara	LOU	12//
160	Gly	Ser	Gln	Pro	Ala	Lys	Leu	GTÄ		Leu	Cys	ser	PIO		Arg	nea	
														275			
161				365	maa	TT 3 3 /	77.07	7C X (370	7070	ייבי ייני	TCCT/	מממי	375 a ਟਾਸਾ	A C C A I	ርርልር ጥ	1333
163				CTC		TAA	GAGA	CGA S		CCAC'	IC T	TCCT(CAAA.		AGCA	CCAG T	1333
163 164			Glu	CTC		TAA	GAGA	CGA (CCAC!	IC T'	TCCT(CAAA		AGCA	CCAG T	1333
163 164 165	Pro	Glu	Glu 380	CTC Leu	Cys				TTGT(A CT			
163 164 165 167	Pro CAC	Glu ACAT	Glu 380 ACC	CTC Leu TGGT	Cys CCTC'	TG A	GTCAG	CCGT	TTGT	GGGT	GTCC	ACA	GCAC	A CTA	AGAT	GCCTTT	1333 1393 1453
163 164 165 167 168	Pro CAC	Glu ACAT.	Glu 380 ACC '	CTC Leu TGGT ACGC	Cys CCTC' TGCT	IG AG	GTCA(CCGT(TTGT(C TG(C CT/	GGGT(AAGG(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393
163 164 165 167 168 169	Pro CAC GTT CCT	Glu ACAT. CGGG TAAA	Glu 380 ACC CAC CTG	CTC Leu TGGT ACGC	Cys CCTC' TGCT CAGG	IG AG	GTCA(CTTT(CCCT(CCGT(CCTT(TTGTO C TGO C CTA G GA	GGGT(AAGG(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171	Pro CAC	Glu ACAT CGGG TAAA INFO	Glu 380 ACC C CAC C CTG C	CTC Leu TGGT ACGC TCCT	Cys CCTC' TGCT CAGG FOR	IG AG GA IG CI CG SEQ	GTCAC CTTT CCCTC	CCGT CCTT CTAT O: 2	TTGTO C TGO C CTA G GAA	GGGT(AAGG(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173	Pro CAC GTT CCT	Glu ACAT CGGG TAAA INFO	Glu 380 ACC CAC CAC C CTG C	CTC Leu TGGT ACGC' TCCT ION	Cys CCTC TGCT CAGG FOR E CH	IG AG GA TG CT CG SEQ ARAC	GTCAC CTTTC CCCTC ID NO	CCGT CCTT CTAT O: 2	TTGTO C TGO C CTA G GAA :	GGGT(AAGG(AAGC(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174	Pro CAC GTT CCT	Glu ACAT CGGG TAAA INFO	Glu 380 ACC C CAC C CTG C RMAT SEQ	CTC Leu TGGT ACGC TCCT ION UENC	Cys CCTC' TGCT CAGG FOR FOR NGTH	IG AG GA TG CT CG SEQ ARACG	GTCAC CTTTC CCCTC ID NO FERI: 2 am.	CCGTCCTATCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TTGTO C TGO C CTA G GAA :	GGGT(AAGG(AAGC(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174	Pro CAC GTT CCT	Glu ACAT CGGG TAAA INFO	Glu 380 ACC CAC CTG CAC RMAT SEQI (A	CTC Leu TGGT ACGC TCCT ION UENC UENC) LE	Cys CCTC IGCT CAGG FOR E CH NGTH PE:	TG AG GA TG CT CG SEQ ARACG : 38	GTCACCTTTCCCCTCID NOTERIS	CCGTCCTATCCTATCCCTATCCCCTATCCCCCCCCCCCC	TTGTO C TGC C CT G GA : S: acid	GGGT(AAGG(AAGC(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175	Pro CAC GTT CCT	Glu ACAT CGGG TAAA INFO	Glu 380 ACC CAC C CTG C RMAT SEQ (A (B	CTC Leu TGGT ACGC TCCT ION UENC) LE) TY) ST	Cys CCTC' TGCT CAGG FOR FOR NGTH	TG AGGA TGCT CGSEQ : 38:amingEDNE	GTCAGCTTTG CCCTG ID NG TERIS 2 am 5 ac SS:	CCGT(CCTT(CTAT(C: 2 STIC(ino) id sing	TTGTO C TGC C CT G GA : S: acid	GGGT(AAGG(AAGC(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174	Pro CACAGTTC CCTT (2)	Glu ACAT CGGG TAAA INFO (i)	Glu 380 ACC CAC CTG CTG CTG (ACC) (ACC) (BC) (CC) (CC) (CC) (CC)	CTC Leu TGGT ACGC ION UENC) LE) TY) ST	Cys CCTC TGCTC CAGG FOR E CH. NGTH PE: RAND POLO	TG AGGA TG SEQ ARAC : 38 amin EDNE	GTCACCTTTCCCTID NOTERING and according SS:	CCGTCCTATCCTATCCCTATCCCCTATCCCCCCCCCCCC	TTGTO C TGC C CT G GA : S: acid	GGGT(AAGG(AAGC(GTCC CCAC	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176	Pro CAC GTT CCT (2)	Glu ACAT. CGGG TAAA INFO (i)	Glu 380 ACC / CAC / CTG / RMAT SEQ (A (B (C (D MOL FRA	CTC Leu IGGT ACGC ION UENC) LE) TY) ST) TO ECUL GMEN	CYS CCTC TGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY	TG AGGA TG SEQ SEQ SARAC'S ARAC'S ABBIT SEDNES GY: PE: PE:	GTCACCTTTCCCTCID NOTERIS among accommodate	CCGTCCTATCCCTATCCCCTATCCCCCCCCCCCCCCCCC	TTGTO C TGC C CT; G GA. : S: acid.	GGGT(AAGC(AAGC(GTCC CCAC GGGG	ACA(GCAC CTCT	A CTA	AGAT(GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180	Pro CAC GTT CCT (2)	Glu ACAT CGGG TAAA INFO (i) (ii) (v) (xi)	Glu 380 ACC CAC CTG RMAT SEQI (A (B (C D MOL FRA	CTC Leu TGGT ACGC TCCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC	CYS CCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE	IG AG GA TO SEQ : ARAC' : 38: amin GY: PE: PE: SCRI	GTCAGCTTTCCCTCID NOTERISCONDENSISTED ACCORDANCES SINCE PTIO	CCGTCCTATCCTATCCCCCCCCCCCCCCCCCCCCCCCCC	TTGTO C TGC C CTG G GA : S: acid le	GGGT(AAGC(S	GTCC CCAC GGGG : 2:	ACA(CAA)	GCAC CTCT GCTA.	TAT A	AGATA AGTA GACC	GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177	Pro CAC GTT CCT (2)	Glu ACAT CGGG TAAA INFO (i) (ii) (v) (xi)	Glu 380 ACC CAC CTG RMAT SEQI (A (B (C D MOL FRA	CTC Leu TGGT ACGC TCCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC	CYS CCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE	IG AGGA TO SEQ : 38: aming GY: PE: 19E: SCRI	GTCAGCTTTCCCTCID NOTERISCONDENSISTED ACCORDANCES SINCE PTIO	CCGTCCTATCCTATCCCCCCCCCCCCCCCCCCCCCCCCC	TTGTO C TGC C CTG G GA : S: acid le	GGGT(AAGC(S	GTCC CCAC GGGG : 2:	ACA(CAA)	GCAC CTCT GCTA.	TAT A	AGATA AGTA GACC	GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182	Pro CAC GTT (CCT (2)	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg	Glu 380 ACC CAC CTG CTG (A (B (C (D MOL FRA SEQ Ser	CTC Leu IGGT ACGC ICCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC Glu	CYS CCTC TGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE Pro	IG AGGA TO SEQ : 38: amino EDNE: GY: PE: SCRI	GTCAGCTTTCCCTCID NOTERISCO access: continued in temperature and the continued access: continued accessive access: continued access: continued access: continued accessive access: continued accessive access: continued accessive access: continued accessive access	CCGTCCTATCCCTATCCCCCCCCCCCCCCCCCCCCCCCC	TTGTO C TGC C CTG G GA : S: acid le EQ I Ala	GGGT(AAGG) AAGC(S D NO Gly 10	GTCC CCAC GGGG : 2: Asn	ACA(CTT)	GCAC CTCT GCTA	TAT AGAA AGG	AGATA AGTA GACC Gly 15	GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184	Pro CAC GTT (CCT (2)	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg	Glu 380 ACC CAC CTG CTG (A (B (C (D MOL FRA SEQ Ser	CTC Leu IGGT ACGC ICCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC Glu	CYS CCTC TGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE Pro	IG AGGA TO SEQ : 38: amino EDNE: GY: PE: SCRI	GTCAGCTTTCCCTCID NOTERISCO access: continued in temperature and the continued access: continued accessive access: continued access: continued access: continued accessive access: continued accessive access: continued accessive access: continued accessive access	CCGTCCTATCCCTATCCCCCCCCCCCCCCCCCCCCCCCC	TTGTO C TGO C CTA G GAA : S: acid le EQ I Ala Val	GGGT(AAGG) AAGC(S D NO Gly 10	GTCC CCAC GGGG : 2: Asn	ACA(CTT)	GCAC CTCT GCTA	TAT AGAA AGG O	AGATA AGTA GACC Gly 15	GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184 185	Pro CAC GTT (CCT (2) Met 1 Thr	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg	Glu 380 ACC CAC CTG RMAT SEQ (A (B (C (D MOL FRA SEQ Ser Val	CTC Leu TGGT ACGC TCCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC Glu Leu 20	CYS CCTC' IGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY E DE Pro 5 Gln	IG AG GA TO CT CO SEQ : 38: amino EDNE: GY: PE: SCRI Thr	GTCAGCTTTCCCCTCID NOTERISCO acceptate protection acceptate protection acceptate accept	CCGTCCTATCCCTATCCCCCTATCCCCCCCCCCCCCCCC	C TGC C CTG G GAA: S: acid le EQ I Ala Val 25	GGGTG AAGCG S D NO Gly 10 Pro	GTCC CCAC GGGG : 2: Asn Ser	ACA(CTT)	GCAC CTCT GCTA Thr	Leu Thr	AGATA AGTA GACC Gly 15 Cys	GCCTTT TCTGTT Val His	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184 185 186	Pro CAC GTT (CCT (2) Met 1 Thr	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg	Glu 380 ACC CAC CTG RMAT SEQ (A (B (C (D MOL FRA SEQ Ser Val	CTC Leu TGGT ACGC TCCT ION UENC) LE) TY) ST) TO ECUL GMEN UENC Glu Leu 20	CYS CCTC' IGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY E DE Pro 5 Gln	IG AG GA TO CT CO SEQ : 38: amino EDNE: GY: PE: SCRI Thr	GTCAGCTTTCCCCTCID NOTERISCO acceptate protection acceptate protection acceptate accept	CCGTCCTATCCTATCCCTATCCCTATCCCCTATCCCCCCCC	C TGC C CTG G GAA: S: acid le EQ I Ala Val 25	GGGTG AAGCG S D NO Gly 10 Pro	GTCC CCAC GGGG : 2: Asn Ser	ACA(CTT)	GCAC CTCT GCTA Thr Glu Val	Leu Thr	AGATA AGTA GACC Gly 15 Cys	GCCTTT TCTGTT	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184 185 186	Pro CAC GTT (CCT (2) Met 1 Thr	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg Ser Ser	Glu 380 ACC CAC CTG RMAT SEQ (A (B (C D MOL FRA SEQ Ser Val Tyr 35	CTC Leu IGGTO ACGC ICCT ION UENC) LE) TY) ST) TO GMEN UENC Glu Leu 20 Glu	CYS CCTC' IGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE Pro 5 Gln Glu	TG AG GA TG CT CG SEQ ARACC: 38: aming EDNE: GY: PE: SCRI Thr Ser	GTCAGCTTTCCCCTCID NOTERISCONDENSING ASSISTANT	CCGTCCTATCCTATCCCTATCCCTATCCCTATCCCTATCCTATCATC	C TGCC CTGG GAA: S: acid le EQ I Ala Val 25 Val	GGGTGAAGCGAAGCGAAGCGAAGCGAAGCGAAGCGAAGC	GTCC CCAC GGGG : 2: Asn Ser Val	ACAA CATTO Thr Ser Val	GCAC CTCT GCTA Thr Glu Val 45	Leu Thr 30	AGATA AGTA GACC Gly 15 Cys Ser	GCCTTT TCTGTT Val His Ala	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184 185 186 187 188	Pro CAC GTT (CCT (2) Met 1 Thr	Glu ACAT CGGG TAAA INFO (ii) (v) (xi) Arg Ser Ser	Glu 380 ACC CAC CTG RMAT SEQ (A (B (C D MOL FRA SEQ Ser Val Tyr 35	CTC Leu IGGTO ACGC ICCT ION UENC) LE) TY) ST) TO GMEN UENC Glu Leu 20 Glu	CYS CCTC' IGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE Pro 5 Gln Glu	TG AG GA TG CT CG SEQ ARACC: 38: aming EDNE: GY: PE: SCRI Thr Ser	GTCACCTTTCCCCTCTID NOTERIS 2 am. co ac SS: contraction to a section to	CCGTCCTATCCTATCCCTATCCCTATCCCTATCCCTATCCTATCATC	C TGCC CTGG GAA: S: acid le EQ I Ala Val 25 Val	GGGTGAAGCGAAGCGAAGCGAAGCGAAGCGAAGCGAAGC	GTCC CCAC GGGG : 2: Asn Ser Val	ACAACTTC Thr Ser Val	GCAC CTCT GCTA Thr Glu Val 45	Leu Thr 30	AGATA AGTA GACC Gly 15 Cys Ser	GCCTTT TCTGTT Val His	1393 1453
163 164 165 167 168 169 171 173 174 175 176 177 180 182 184 185 186 187 188	Pro CAC GTT (CCT (2) Met 1 Thr Val	Glu ACAT CGGG IAAA INFO (ii) (v) (xi) Arg Ser Ser Cys 50	Glu 380 ACC CAC CTG RMAT SEQ (A (B (C (D MOL FRA SEQ Ser Val Tyr 35 Leu	CTC Leu IGGT ACGC ICCT ION UENC) LE) TY) TO ECUL GMEN UENC Glu Leu 20 Glu Leu Leu	Cys CCTC' IGCTC CAGG FOR E CH. NGTH PE: RAND POLO E TY T TY E DE Pro 5 Gln Glu	TG AG GA TG CT CG SEQ : 38: aming EDNE: GY: PE: SCRI Thr Ser Leu	GTCACCTTTCCCCTCID NOTERISCONDENSISTED ACCESS: 100 access of the proteinte PTIONARD Arguments Arg	CCGTCCTATCCTATCCCTATCCCTATCCCTATCCCCTATCCCCTATCCCCTATCCCCTATCCCCTATCCCTATCCCCTATCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCCCTATCATC	TTGTO C TGC C CTA G GAA : S: acid le EQ I Ala Val 25 Val Asn	GGGTGAAGGGAAGGGGS D NO Gly 10 Pro Leu Cys	GTCC CCAC GGGG : 2: Asn Ser Val Leu	ACAACTTC Thr Ser Val Thr 60	GCAC CTCT GCTA Thr Glu Val 45 Ala	Leu Thr 30 Tyr	Gly 15 Cys Ser	GCCTTT TCTGTT Val His Ala	1393 1453



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,470

DATE: 11/20/2001
TIME: 19:11:34

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\I836470.raw

193	65					70					75					80
194	LOU	Car	T.011	Cvs	Glu		Leu	Tvr	Ile	Ser	Thr	Val	Pro	Leu	Trp	Ile
195	Leu	Ser	БСи	Cys	85	Lou		-1-		90					95	
196	T1_0	Tvr	Tle	Gln		Gln	His	Lvs	Trp	Asn	Leu	Gly	Pro	Gln	Ala	Cys
197	110	- 1 -	110	100					105			_		110		
198	Lvc	Val	Thr	Δla	Tur	Tle	Phe	Phe	Cys	Asn	Ile	Tyr	Ile	Ser	Ile	Leu
199	цуз	Val	115	11.14	+1-			120	- 1			-	125			
200	T.OH	T.011	Cvs	Cvs	Tle	Ser	Cvs	Asp	Arg	Tyr	Met	Ala	Val	Val	Tyr	Ala
201	пси	130	010	0,12			135	-	_	-		140				
202	T.e.II	Glu	Ser	Ara	Glv	His	Arq	His	Gln	Arg	Thr	Ala	Val	Thr	Ile	Ser
203	145	0		5	1	150	,			_	155					160
204	Ala	Cvs	Va l	Ile	Leu	Leu	Val	Gly	Leu	Val	Asn	Tyr	Pro	Val	Phe	Asp
205					165					170					175	
206	Met	Lvs	Val	Glu	Lys	Ser	Phe	Cys	Phe	Glu	Pro	Leu	Arg	Met	Asn	Ser
207				180					185					190		
208	Lvs	Ile	Ala	Gly	Tyr	His	Tyr	Leu	Arg	Phe	Thr	Phe	Gly	Phe	Ala	Ile
209			195					200					205			
210	Pro	Leu	Gly	Ile	Leu	Ala	Phe	Thr	Asn	His	Gln	Ile	Phe	Arg	Ser	Ile
211		210					215					220				
212	Lvs	Leu	Ser	Asp	Ser	Leu	Ser	Ala	Ala	Gln	Lys	Asn	Lys	Val	Lys	Arg
213	225					230					235					240
214	Ser	Ala	Ile	Ala	Val	Val	Thr	Ile	Phe	Leu	Val	Cys	Phe	Ala	Pro	Tyr
215					245					250					255	
216	His	Val	Val	Leu	Leu	Val	Lys	Ala	Ala	Ser	Phe	Ser	Phe	Tyr	Gln	Gly
217				260					265					270		
218	Asp	Met	Asp	Ala	Val	Cys	Ala	Phe	Glu	Ser	Arg	Leu	Tyr	Thr	Val	Ser
219			275					280					285			
220	Met	Val	Phe	Leu	Cys	Leu	Ser	Thr	Val	Asn	Ser		Ala	Asp	Pro	IIe
221		290					295				_	300	•	_	_	-1-
222	Ile	Tyr	Val	Leu	Gly	Thr	Asp	His	Ser	Arg		Glu	Val	Ser	Arg	TTE
223	305					310					315	_	7	m1	a	320
224	His	Thr	Gly	\mathtt{Trp}		Lys	${\tt Trp}$	Ser	Thr	Lys	Thr	Tyr	vaı	Tnr	Cys	ser
225					325				_	330		_	a	3	335	Ш.т.
226	Lys	Asp	Ser		Glu	Thr	His	Leu	Pro	Thr	Glu	Leu	ser	ASI	THE	IÀT
227				340			•	_	345	a 1	a	<i>a</i> 1	Dwo	350	T ***	LOU
228	Thr	Phe			Pro	Ala	His		Pro	GIY	ser	GIII	265	АІа	гуз	Leu
229			355		_	_	~ 1	360	T	Dana	<i>α</i> 1	Cl.,	365			
230	Gly			Cys	Ser	Pro			Leu	Pro	GIU	380	теп	Cys		
231		370					375					360				
	(2)	INFO	RMAT	TON	FOR	SEQ	TD N	O: 3	: c.							
235		(i)	SEQ	UENC	E CH	ARAC	TERL	STIC	5: ~~i~	<u> </u>						
236			(A) LE	NGTH	: 29	38 D	ase asid	pair	5						
237			(B) TY	PE:	nucl	erc.	acina	1.0							
238						EDNE GY:			Te							
239																
241						PE:	Orne	_		•						
242		(1X)	FEA	TOKE	МЕ /Р	гv.	COdi	na S	eque	nce						
244						ON:										
245			(B	J LO	CHII	ON.	JU1.	20	10							





DATE: 11/20/2001

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,470

TIME: 19:11:34

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\1836470.raw

246			(D)	отн	ER I	NFOF	MATI	ON:									
248	(xi)	SEQU	ENCE	DES	CRIF	TION	: SE	Q ID	NO:	3:			•			
250	GGGA	GGGG	TG C	NANG	CTAG	C CA	CGCA	GGCG	GGG	CCCT	GGG	TCAT	TTTA	AN C	TCTC	AGAGT	60
251	GAAC	GTCT	TG A	TAGG	ACCG	A CA	ANAC	CNCAT	NAC	NTGT	ACT	TAGA	TAGO	TT A	TCTT	ANANC	120
252	CACN	CTGA	NA T	TGGA	ACCC	G CA	LAAAI	ATGC	CNG	GGAG	GAA	GGTG	AGCA	AG G	GACA	.CGACA	180
253	CTCA	CCCG	GA T	AAAC	CCAA	C AA	GCGC	CAGCG	AGG	CTGT	GGG	GAAA	CCGG	SAN C	CCTG	CACAC	240
254	CGCC	GGGG	GA A	GGTG	GGCC	N CC	CGCCA	CCAC	CGI	GGAA	GAA.	CAGC	GCGG	AN C	CACC	CCACG	300
255	AGAT	GAGA	CG G	AACI	GCCG	T GP	GATO	CCAGC	CAAT	NCCN	ACT	GTGG	GTCT	GA C	CCAG	GATAN	360
256	CGGA	AAGC	CAG G	GACG	TGAA	C AC	CCCI	CCTC	ATO	TTCT	TGA	CACC	GTCA	ATT C	CTCAG	CAGCT	420
257	CAGC	TAAC	GC A	CAGA	AGGCA	G CC	GAGC	CGTCT	GTC	CAGCA	GAG	TCGT	GGCI	GA C	CAGA	ACACG	480
258	CCAC	ACGC	CA C	ACGC	CACA	C GC	CACA	ACGTO	CAG	GATI	GCT	CAAG	ATGO	SAA G	GGCA	CAGTG	540
259	GAAT	'ATA'	AT A	TATA	TTTA	CA TA	TTTT	GGCG	AGA	CCCI	GGA	GGAC	CACAC	CTG A	ATAC	AATGG	600
260	AATA	CCAT	CC C	GCC1	TTGA	A AC	GAAG	GGAA	ATC	CCTGG	CAC	ACGC	TGC	AAC A	AGGAG	GGAGC	660
261	TTGA	GGAC	CAC I	GTGG	TGAC	ST GO	SAGC	ACGTO	G AGA	CACG	GAA	GGAC	CACAC	CGC 'I	GAAG	ACACG	720
262	CAGA	GATO	CC C	CACCO	CACGI	G GC	GAGG	STGAC	AGG	GGAG	CCC	AGCG	CAC	AGA G	SACAA	AGTGG	780
263	AATO	GAGG	CC I	GGGG	GCT	G G	AGCA	AATGO	GGA	AGCGA	GTG	CTTC	CTGG	GG C	CAGAG	TCTCC	840
264	GTTT	'GGG <i>E</i>	AG A	TGAC	GAAGO	ST TO	CTGCC	CGACG	GAT	GCTG	GCG	ATGO	TTGC	CAG	AAGAA	TGTGA	900
265	ATO	TGC	CCA	ATC	CTA	A CTO	AAA	A AAC	G GG1	TAC	: AA:	r GG <i>F</i>	AAC	GCC	ACC	CCA	948
266	Met	. Cys	s Pro	Met	: Lei	ı Let	ı Lys	s Asr	ı Gl		Asr	ı GIZ	Asr) Ala	a Tnr	Pro	
267	1				5					10					15	3.00	006
269	GTG	ACC	ACC	ACT	GCC	CCG	TGG	GCC	TCC	CTG	GGC	CTC	TCC	GCC	AAG	ACC	996
270	Val	Thr	Thr		Ala	Pro	${\tt Trp}$	Ala		Leu	GLY	Leu	Ser		ьys	Thr	
271				20					25					30	ama	ama.	1044
273	TGC	AAC	AAC	GTG	TCC	TTC	GAA	GAG	AGC	AGG	ATA	GTC	CTG	GTC	GTG	GTG	1044
274	Cys	Asn	Asn	Val	Ser	Phe	Glu	Glu	Ser	Arg	He	Val	Leu	vaı	vaı	vai	,
275			35					40			~ ~ ~		45	ата	3 Cm	000	1092
27.7	TAC	AGC	GCG	GTG	TGC	ACG	CTG	GGG	GTG	CCG	GCC	AAC	TGC	CTG	ACT	Ala	1092
278	${ t Tyr}$	Ser	Ala	Val	Cys	Thr		Gly	Val	Pro	Ата		Cys	ьeu	THI	Ald	
279		50					55					60	ama	000	CITIC.	ma C	1140
281	TGG	CTG	GCG	CTG	CTG	CAG	GTA	CTG	CAG	GGC	AAC	GTG	CTG	312	Unl	TAC	1140
282	_	Leu	Ala	Leu	Leu		Val	Leu	GIN	GIĀ		vai	Leu	Ald	val	80	
283	65					70			ama	ama	75	202	aaa	7.00	cmc		1188
285	CTG	CTC	TGC	CTG	GCA	CTC	TGC	GAG	CTG	CTG	TAC	ACA mb~	Clar	Mbx	Tou	CCA .	1100
286	Leu	Leu	Cys	Leu		Leu	Cys	Glu	ьeu	90	тут	1111	СТУ	1111	95	FIO	
287					85	3.55	000	7 7 C	C A C	-	CCC	TCC	אככ	CTD		CTG	1236
289	CTC	TGG	GTC	ATC	TAT	ATC	CGC	AAC	CAG	UAC	Ara	mrn	Thr	LOU	Glv	T.en	1230
290	Leu	Trp	Val		туr	ше	Arg	Asn	105	птэ	Arg	115	1111	110	Ory	Dea	
291				100	ama	3.00	aaa	TAC		መመረ	mmC	TCC	አልሮ		ጥልሮ	GTC	1284
293	CTG	GCC	TGC	AAG	GTG	ACC	Ala	Tyr	TIO	Dho	Dho	Cve	Agn	Tle	Tur	Val	1201
294	Leu	Ala		ьуs	vaı	THE	Ата	120	116	Pne	PHE	Суз	125	110	- 1 -	, 44	
295			115	mm.a	ama	maa	maa		TH CHC	TCC	CAC	CCC		стс	GCC	GTG	1332
297	AGC	ATC	CTC	TTC	CTG	TGC	TGC	ATC	Cor	CAC	Acn	Ara	Dhe	Val	Δla	Val	1002
298	Ser		ьeu	Pne	Leu	Cys		Ile	Ser	Суз	АЗР	140	FIIC	Vul	1114	, u.	
299	a===	130	000	OEC.	CAC	y Cam	135	GGC	CCC	CCC	CGC		AGG	ACC	GCC	АТС	1380
301	GTG	TAC	GCG	CTG	GAG	AGT	7 ~~	C1	λ ~~	Δ r.α	Ara	Δrα	Ara	Thr	Ala	Tle	
302		тyr	ата	ьeu	GIU	150	AIG	Gly	лту	пту	155	тту	1119	T 11T		160	
303	145	3 m.~	maa	000	шсс		mm.c	ATC	CTC	ርጥር			G TT	CAC	ТАС		1428
305	CTC	ATC	TCC	GCC 77 ~	760	AIC	Dho	Ile	T.Au	Val	G1 tr	Tle	Val	His	Tvr	Pro	
306	Leu	тте	ser	ата	cys	тте	FIIG	тте	ьeu	val	ату	116	, aı	1113	-1-		





VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,470

DATE: 11/20/2001 TIME: 19:11:35

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\1836470.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]